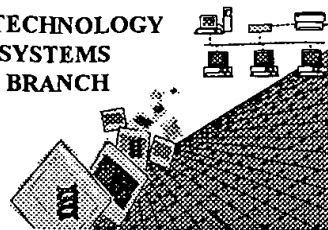


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/943,944
Source: O/P E
Date Processed by STIC: 1/31/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/943,944

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIKE

RAW SEQUENCE LISTING

DATE: 01/31/2002

PATENT APPLICATION: US/09/943,944

TIME: 12:56:30

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\01312002\I943944.raw

SEQUENCE LISTING

Does Not Comply
Corrected Diskette Needed

pg 2-6

4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: Ptashne, Mark
 7 Xiangyang, Lu
 8 Yibing, Wu
 10 (ii) TITLE OF INVENTION: Transcriptional Activation System,
 11 Activators, and Uses Therefor
 13 (iii) NUMBER OF SEQUENCES: 238
 15 (iv) CORRESPONDENCE ADDRESS: *a (use lower-case letter)*
 16 (A) ADDRESSEE: Choate, Hall & Stewart
 17 (B) STREET: 53 State Street
 18 (C) CITY: Boston
 19 (D) STATE: MA
 20 (E) COUNTRY: USA
 21 (F) ZIP: 02109
 23 (v) COMPUTER READABLE FORM:
 24 (A) MEDIUM TYPE: Floppy disk
 25 (B) COMPUTER: IBM PC compatible
 26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 29 (vi) CURRENT APPLICATION DATA:
 C--> 30 (A) APPLICATION NUMBER: US/09/943,944
 C--> 31 (B) FILING DATE: 07-Jan-2002
 32 (C) CLASSIFICATION:
 34 (viii) ATTORNEY/AGENT INFORMATION:
 35 (A) NAME: Jarrell Ph.D., Brenda H
 36 (B) REGISTRATION NUMBER: 39,223
 37 (C) REFERENCE/DOCKET NUMBER: 0342941-0065
 39 (ix) TELECOMMUNICATION INFORMATION:
 40 (A) TELEPHONE: 617 248 5000
 41 (B) TELEFAX: 617 248 4000

ERRORED SEQUENCES

65 (2) INFORMATION FOR SEQ ID NO: 2:
 67 (i) SEQUENCE CHARACTERISTICS: *p.2*
 68 (A) LENGTH: 18 base pairs
 69 (B) TYPE: nucleic acid
 70 (C) STRANDEDNESS: not relevant
 71 (D) TOPOLOGY: not relevant
 73 (ii) MOLECULE TYPE: DNA (genomic)
 75 (vi) ORIGINAL SOURCE:

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/943,944

DATE: 01/31/2002
TIME: 12:56:30

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\01312002\I943944.raw

76 (C) INDIVIDUAL ISOLATE: LS1 DNA sequence
80 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
E--> 82 CCCCTCTTNN CNNCCCTC → 18 (global format error - see item 1 on Enrol
W--> 83 18 summary sheet)
85 (2) INFORMATION FOR SEQ ID NO: 3:
87 (i) SEQUENCE CHARACTERISTICS:
88 (A) LENGTH: 18 base pairs
89 (B) TYPE: nucleic acid
90 (C) STRANDEDNESS: not relevant
W--> 91 (D) TOPOLOGY: not relevant
93 (ii) MOLECULE TYPE: DNA (genomic)
96 (vii) IMMEDIATE SOURCE:
97 (B) CLONE: LS2 DNA sequence
101 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3: same error
E--> 103 ATTCCGCCAC CGTATTTTC
W--> 104 18
127 (2) INFORMATION FOR SEQ ID NO: 5:
129 (i) SEQUENCE CHARACTERISTICS:
130 (A) LENGTH: 18 base pairs
131 (B) TYPE: nucleic acid
132 (C) STRANDEDNESS: not relevant
W--> 133 (D) TOPOLOGY: not relevant
135 (ii) MOLECULE TYPE: DNA (genomic)
138 (vii) IMMEDIATE SOURCE:
139 (B) CLONE: LS3 DNA sequence
143 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5: same
E--> 145 CTGCCCCGGGT GTTCTCTTC
W--> 146 18
169 (2) INFORMATION FOR SEQ ID NO: 7:
171 (i) SEQUENCE CHARACTERISTICS:
172 (A) LENGTH: 18 base pairs
173 (B) TYPE: nucleic acid
174 (C) STRANDEDNESS: not relevant
W--> 175 (D) TOPOLOGY: not relevant
177 (ii) MOLECULE TYPE: DNA (genomic)
180 (vii) IMMEDIATE SOURCE:
181 (B) CLONE: LS4 DNA sequence
185 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7: same
E--> 187 CAGCTCCCCC CCTGGTTA
W--> 188 18
211 (2) INFORMATION FOR SEQ ID NO: 9:
213 (i) SEQUENCE CHARACTERISTICS:
214 (A) LENGTH: 18 base pairs
215 (B) TYPE: nucleic acid
216 (C) STRANDEDNESS: not relevant
W--> 217 (D) TOPOLOGY: not relevant
219 (ii) MOLECULE TYPE: DNA (genomic)
222 (vii) IMMEDIATE SOURCE:
223 (B) CLONE: LS5 DNA SEQUENCE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/943,944

DATE: 01/31/2002
TIME: 12:56:30

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\01312002\I943944.raw

227 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
E--> 229 TACTGGCCCT CCCCCTTC
W--> 230 18
253 (2) INFORMATION FOR SEQ ID NO: 11:
255 (i) SEQUENCE CHARACTERISTICS:
256 (A) LENGTH: 18 base pairs
257 (B) TYPE: nucleic acid
258 (C) STRANDEDNESS: not relevant
W--> 259 (D) TOPOLOGY: not relevant
261 (ii) MOLECULE TYPE: DNA (genomic)
264 (vii) IMMEDIATE SOURCE:
265 (B) CLONE: LS6 DNA SEQUENCE
269 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
E--> 271 GAGTCCCCCT ATGACTTG
W--> 272 18
295 (2) INFORMATION FOR SEQ ID NO: 13:
297 (i) SEQUENCE CHARACTERISTICS:
298 (A) LENGTH: 18 base pairs
299 (B) TYPE: nucleic acid
300 (C) STRANDEDNESS: not relevant
W--> 301 (D) TOPOLOGY: not relevant
303 (ii) MOLECULE TYPE: DNA (genomic)
306 (vii) IMMEDIATE SOURCE:
307 (B) CLONE: LS7 DNA SEQUENCE
311 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
E--> 313 ACCGCCGAAT TCCCCCTC
W--> 314 18
337 (2) INFORMATION FOR SEQ ID NO: 15:
339 (i) SEQUENCE CHARACTERISTICS:
340 (A) LENGTH: 18 base pairs
341 (B) TYPE: nucleic acid
342 (C) STRANDEDNESS: not relevant
W--> 343 (D) TOPOLOGY: not relevant
345 (ii) MOLECULE TYPE: DNA (genomic)
348 (vii) IMMEDIATE SOURCE:
349 (B) CLONE: LS8 DNA SEQUENCE
353 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
E--> 355 CAATTTCTAG ACGCACTT
W--> 356 18
379 (2) INFORMATION FOR SEQ ID NO: 17:
381 (i) SEQUENCE CHARACTERISTICS:
382 (A) LENGTH: 18 base pairs
383 (B) TYPE: nucleic acid
384 (C) STRANDEDNESS: not relevant
W--> 385 (D) TOPOLOGY: not relevant
387 (ii) MOLECULE TYPE: DNA (genomic)
390 (vii) IMMEDIATE SOURCE:
391 (B) CLONE: LS9 DNA sequence
395 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/943,944

DATE: 01/31/2002
TIME: 12:56:30

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\01312002\I943944.raw

E--> 397 ACATTCCTG ACCCTTC
W--> 398 18
421 (2) INFORMATION FOR SEQ ID NO: 19:
423 (i) SEQUENCE CHARACTERISTICS:
424 (A) LENGTH: 18 base pairs
425 (B) TYPE: nucleic acid
426 (C) STRANDEDNESS: not relevant
W--> 427 (D) TOPOLOGY: not relevant
429 (ii) MOLECULE TYPE: DNA (genomic)
432 (vii) IMMEDIATE SOURCE:
433 (B) CLONE: LS10 DNA sequence
437 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:
E--> 439 ATCGGCCCAN CNCTTTC
W--> 440 18
442 (2) INFORMATION FOR SEQ ID NO: 20:
444 (i) SEQUENCE CHARACTERISTICS:
445 (A) LENGTH: 18 base pairs
446 (B) TYPE: nucleic acid
447 (C) STRANDEDNESS: not relevant
W--> 448 (D) TOPOLOGY: not relevant
450 (ii) MOLECULE TYPE: DNA (genomic)
453 (vii) IMMEDIATE SOURCE:
454 (B) CLONE: LS11 DNA sequence
458 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:
E--> 460 TTGGATTTT CCTACGTC
W--> 461 18
484 (2) INFORMATION FOR SEQ ID NO: 22:
486 (i) SEQUENCE CHARACTERISTICS:
487 (A) LENGTH: 18 base pairs
488 (B) TYPE: nucleic acid
489 (C) STRANDEDNESS: not relevant
W--> 490 (D) TOPOLOGY: not relevant
492 (ii) MOLECULE TYPE: DNA (genomic)
495 (vii) IMMEDIATE SOURCE:
496 (B) CLONE: LS12 DNA sequence
500 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:
E--> 502 CCCCCACCAC CCTGGCCC
W--> 503 18
526 (2) INFORMATION FOR SEQ ID NO: 24:
528 (i) SEQUENCE CHARACTERISTICS:
529 (A) LENGTH: 18 base pairs
530 (B) TYPE: nucleic acid
531 (C) STRANDEDNESS: not relevant
W--> 532 (D) TOPOLOGY: not relevant
534 (ii) MOLECULE TYPE: DNA (genomic)
537 (vii) IMMEDIATE SOURCE:
538 (B) CLONE: LS13 DNA sequence
542 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:
E--> 544 CTCTTTGAAT GAGGAACC

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/943,944

DATE: 01/31/2002
TIME: 12:56:30

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\01312002\I943944.raw

W--> 545 18
568 (2) INFORMATION FOR SEQ ID NO: 26:
570 (i) SEQUENCE CHARACTERISTICS:
571 (A) LENGTH: 18 base pairs
572 (B) TYPE: nucleic acid
573 (C) STRANDEDNESS: not relevant
W--> 574 (D) TOPOLOGY: not relevant
576 (ii) MOLECULE TYPE: DNA (genomic)
579 (vii) IMMEDIATE SOURCE:
580 (B) CLONE: LS14 DNA sequence
584 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:
E--> 586 CTGCTCGACA TACCTTTC
W--> 587 18
610 (2) INFORMATION FOR SEQ ID NO: 28:
612 (i) SEQUENCE CHARACTERISTICS:
613 (A) LENGTH: 18 base pairs
614 (B) TYPE: nucleic acid
615 (C) STRANDEDNESS: not relevant
W--> 616 (D) TOPOLOGY: not relevant
618 (ii) MOLECULE TYPE: DNA (genomic)
621 (vii) IMMEDIATE SOURCE:
622 (B) CLONE: LS15 DNA SEQUENCE
626 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:
E--> 628 CTCCCCGACG CCTTCTC
W--> 629 18
652 (2) INFORMATION FOR SEQ ID NO: 30:
654 (i) SEQUENCE CHARACTERISTICS:
655 (A) LENGTH: 18 base pairs
656 (B) TYPE: nucleic acid
657 (C) STRANDEDNESS: not relevant
W--> 658 (D) TOPOLOGY: not relevant
660 (ii) MOLECULE TYPE: DNA (genomic)
663 (vii) IMMEDIATE SOURCE:
664 (B) CLONE: LS16 DNA SEQUENCE
668 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:
E--> 670 CTCTTCCCCG ACCTCAAC
W--> 671 18
694 (2) INFORMATION FOR SEQ ID NO: 32:
696 (i) SEQUENCE CHARACTERISTICS:
697 (A) LENGTH: 18 base pairs
698 (B) TYPE: nucleic acid
699 (C) STRANDEDNESS: not relevant
W--> 700 (D) TOPOLOGY: not relevant
702 (ii) MOLECULE TYPE: DNA (genomic)
705 (vii) IMMEDIATE SOURCE:
706 (B) CLONE: LS17 DNA SEQUENCE
710 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:
E--> 712 TCTTGTTTG ATGTCGAA
W--> 713 18

same

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/943,944

DATE: 01/31/2002
TIME: 12:56:30

Input Set : A:\PTO.VSK.txt
Output Set: N:\CRF3\01312002\I943944.raw

```

736 (2) INFORMATION FOR SEQ ID NO: 34:
738     (i) SEQUENCE CHARACTERISTICS:
739         (A) LENGTH: 18 base pairs
740         (B) TYPE: nucleic acid
741         (C) STRANDEDNESS: not relevant
W--> 742         (D) TOPOLOGY: not relevant
744     (ii) MOLECULE TYPE: DNA (genomic)
747     (vii) IMMEDIATE SOURCE:
748         (B) CLONE: LS18 DNA SEQUENCE
752     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:
E--> 754 CTTGAACCTC CGCCCTGG
W--> 755 18
778 (2) INFORMATION FOR SEQ ID NO: 36:
780     (i) SEQUENCE CHARACTERISTICS:
781         (A) LENGTH: 18 base pairs
782         (B) TYPE: nucleic acid
783         (C) STRANDEDNESS: not relevant
W--> 784         (D) TOPOLOGY: not relevant
786     (ii) MOLECULE TYPE: DNA (genomic)
789     (vii) IMMEDIATE SOURCE:
790         (B) CLONE: LS19 DNA SEQUENCE
794     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:
E--> 796 CAGCTACCTG ATCTGTTC
W--> 797 18
820 (2) INFORMATION FOR SEQ ID NO: 38:
822     (i) SEQUENCE CHARACTERISTICS:
823         (A) LENGTH: 18 base pairs
824         (B) TYPE: nucleic acid
825         (C) STRANDEDNESS: not relevant
W--> 826         (D) TOPOLOGY: not relevant
828     (ii) MOLECULE TYPE: DNA (genomic)
831     (vii) IMMEDIATE SOURCE:
832         (B) CLONE: LS20 DNA SEQUENCE
836     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:
E--> 838 CCTCTCCCAG ACCTCTTC
W--> 839 18

```

same

same

same



The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

VERIFICATION SUMMARY

DATE: 01/31/2002

PATENT APPLICATION: US/09/943,944

TIME: 12:56:32

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\01312002\I943944.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:50 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=1
L:71 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=2
L:82 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:2
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:91 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=3
L:103 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:3
L:104 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:112 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4
L:133 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=5
L:145 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:5
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:154 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=6
L:175 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=7
L:187 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:7
L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:196 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=8
L:217 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=9
L:229 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:9
L:230 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
L:238 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=10
L:259 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=11
L:271 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:11
L:272 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11
L:280 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=12
L:301 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=13
L:313 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:13
L:314 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:322 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=14
L:343 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=15
L:355 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:15
L:356 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:15
L:364 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=16
L:385 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=17
L:397 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:17
L:398 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17
L:406 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=18
L:427 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=19
L:439 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:19
L:440 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:448 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=20
L:460 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:20
L:461 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20
L:469 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=21
L:490 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=22
L:502 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:22
L:503 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22

VERIFICATION SUMMARY

DATE: 01/31/2002

PATENT APPLICATION: US/09/943,944

TIME: 12:56:32

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\01312002\I943944.raw

L:511 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=23
L:532 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=24
L:544 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:24
L:545 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:24
L:553 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=25
L:574 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=26
L:586 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:26
L:587 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26
L:595 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=27
L:616 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=28
L:628 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:28
L:629 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:28
L:637 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=29
L:658 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=30
L:670 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:30
L:671 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:30
L:679 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=31
L:700 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=32
L:712 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:32
L:713 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32
L:721 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=33
L:742 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=34
L:754 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:34
L:755 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:34
L:763 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=35
L:784 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=36
L:796 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:36
L:797 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:36
L:805 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=37
L:826 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=38
L:838 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:38
L:839 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:38
L:847 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=39
L:868 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=40
L:880 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:40
L:881 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:40
L:889 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=41
L:901 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:41
L:902 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:41
L:910 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=42
L:922 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:42
L:923 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:42
L:931 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=43
L:952 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=44
L:964 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:44
L:965 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:44
L:973 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=45
L:994 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=46
L:1006 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:46

VERIFICATION SUMMARY

DATE: 01/31/2002

PATENT APPLICATION: US/09/943,944

TIME: 12:56:32

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\01312002\I943944.raw

L:1007 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46
L:1015 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=47
L:1036 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=48
L:1048 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:48
L:1049 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:48
L:1057 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=49
L:1078 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=50
L:1090 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:50
L:1091 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:50
L:1132 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:52
L:1133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52
L:1174 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:54
L:1175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:54
L:1216 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:56
L:1217 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:56
L:1258 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:58
L:1259 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:58
L:1300 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:60
L:1301 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:60
L:1342 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:62
L:1343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:62
L:1384 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:64
L:1385 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:64
L:1426 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:66
L:1427 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:66
L:1468 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:68
L:1469 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:68
L:1510 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:70
L:1511 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:70
L:1552 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:72
L:1553 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:72
L:1594 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:74
L:1595 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:74
L:1636 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:76
L:1637 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:76
L:1678 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:78
L:1679 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:78
L:1720 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:80
L:1721 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:80
L:1762 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:82
L:1763 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:82
L:1804 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:84
L:1805 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:84
L:1846 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:86
L:1847 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:86
L:1888 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:88
L:1889 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:88
L:1930 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:90
L:1931 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:90

VERIFICATION SUMMARY

DATE: 01/31/2002

PATENT APPLICATION: US/09/943,944

TIME: 12:56:32

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\01312002\I943944.raw

L:1972 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:92
L:1973 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:92
L:2014 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:94
L:2015 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:94
L:2056 M:254 E: No. of Bases conflict, Input:0 Counted:18 SEQ:96
L:2057 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:96

STATISTICS SUMMARY

PATENT APPLICATION: US/09/943,944

DATE: 01/31/2002

TIME: 12:56:32

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\01312002\I943944.raw

Application Serial Number: US/09/943,944

Alpha or Numeric: Alpha

Application Class:

Application File Date: 01-07-2002

Art Unit: OIPE

Software Application: PatentIN1.0

Total Number of Sequences: 238

Total Nucleotides: 2235

Total Amino Acids: 828

Number of Errors: 114

Number of Warnings: 352

Number of Corrections: 0

MESSAGE SUMMARY

246 W: 238 (Invalid value of Alpha Sequence Header Field)

254 E: 114 (No. of Bases conflict)

336 W: 114 (Invalid Amino Acid Number in Coding Region)